<110> Bayer BioScience N.V.
        De Block, Marc

<120> Methods and means for increasing the tolerance of plants to stress conditions.

<130> BCS 03 2002 WO1

<150> PCT/EP04/003995
<151> 2004-04-09

<150> EP03076044.1
<151> 2003-04-09

<150> US 60/496,688
<151> 2003-08-21

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<170> PatentIn version 3.1

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Glu Leu Ile Asp Glu Lys Glu Ser Lys Arg Trp Phe Asp Glu Ile Ile
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Gln Val Leu Phe Leu Ala Ile Ser Asp Ile Arg Asn Ser Leu Ser Leu
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Pro Asp Ser Ser Ile Ser Ser Ser Ala Ser Asp Gly Phe Ser Leu Leu
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Phe Asp Asp Leu Ile Pro Arg Asp Glu Ala Val Lys Trp Phe Lys Glu
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Val Val Pro Lys Met Ala Asp Leu Leu Leu Arg Leu Pro Ser Leu Leu
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12

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13

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14

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15

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Xaa Xaa Xaa Gln
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<221>  MISC_FEATURE
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<220>
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1               5                   10


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<212>  PRT
<213>  Artificial Sequence

<220>
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<220>
<221>  MISC_FEATURE
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<400>  13

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gtg ctc cgc ggc ggc gcg ctc ttc tgg ccg ccg gcg gcg cag gag gcg   96
Val Leu Arg Gly Gly Ala Leu Phe Trp Pro Pro Ala Ala Gln Glu Ala
                20   25   30

ctc aag gcg ctg gcg ctg ggc ccc gac gtg agc cgc gtc tcc tcc ggc   144
Leu Lys Ala Leu Ala Leu Gly Pro Asp Val Ser Arg Val Ser Ser Gly
            35   40   45

gac gtc ctc gcc gac gcc ctc acc gac ctc cgc ctc gcg ctc aac ctc   192
Asp Val Leu Ala Asp Ala Leu Thr Asp Leu Arg Leu Ala Leu Asn Leu
        50   `   55   60

gac cca ctc ccg cgc cgc gcc gcc gag ggc ttc gcg ctc ttc ttc gac   240
Asp Pro Leu Pro Arg Arg Ala Ala Glu Gly Phe Ala Leu Phe Phe Asp
65   70   75   80

gac ctc ctg tcg cgg gcg cag gcg cgg gac tgg ttc gac cac gtc gcc   288
Asp Leu Leu Ser Arg Ala Gln Ala Arg Asp Trp Phe Asp His Val Ala
                85   90   95

19

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ccc tcc ctc gcc cgc ctc ctc ctc cgc ctc ccc acg ctg ctc gag ggc      336
Pro Ser Leu Ala Arg Leu Leu Leu Arg Leu Pro Thr Leu Leu Glu Gly
            100                 105                 110

cac tac cgc gcc gcc ggc gac gag gct cgc ggg ctc cgc atc ctg agc      384
His Tyr Arg Ala Ala Gly Asp Glu Ala Arg Gly Leu Arg Ile Leu Ser
            115                 120                 125

tcg cag gat gcc ggg ctc gtg ctc ctc agc cag gag ctc gcc gcc gcg      432
Ser Gln Asp Ala Gly Leu Val Leu Leu Ser Gln Glu Leu Ala Ala Ala
            130                 135                 140

ctg ctc gcc tgc gcg ctc ttc tgc ctg ttc ccc acc gcc gat agg gcc      480
Leu Leu Ala Cys Ala Leu Phe Cys Leu Phe Pro Thr Ala Asp Arg Ala
145                 150                 155                 160

gag gcg tgc ctc ccg gcg atc aat ttc gat agc cta ttt gcg gca ctg      528
Glu Ala Cys Leu Pro Ala Ile Asn Phe Asp Ser Leu Phe Ala Ala Leu
                165                 170                 175

tgt tat aat tcg agg caa agc cag gag cag aag gtg agg tgc ctt gtt      576
Cys Tyr Asn Ser Arg Gln Ser Gln Glu Gln Lys Val Arg Cys Leu Val
            180                 185                 190

cac tat ttt gac agg gtg acc gct tct aca cct act ggt tcc gtt tcg      624
His Tyr Phe Asp Arg Val Thr Ala Ser Thr Pro Thr Gly Ser Val Ser
            195                 200                 205

ttt gag cgt aag gtt ctt cct cgc cgt cct gaa tct gat ggc att acg      672
Phe Glu Arg Lys Val Leu Pro Arg Arg Pro Glu Ser Asp Gly Ile Thr
            210                 215                 220

tac cct gac atg gat act tgg atg aaa tct ggt gtt ccc ctt tgc aca      720
Tyr Pro Asp Met Asp Thr Trp Met Lys Ser Gly Val Pro Leu Cys Thr
225                 230                 235                 240

ttc cgg gta ttt tcc tca ggc ttg ata gaa gat gag gaa caa gaa gcc      768
Phe Arg Val Phe Ser Ser Gly Leu Ile Glu Asp Glu Glu Gln Glu Ala
                245                 250                 255

ctt gaa gtt gac ttt gca aat aga tat ttg gga ggt ggc gca ctt tcc      816
Leu Glu Val Asp Phe Ala Asn Arg Tyr Leu Gly Gly Gly Ala Leu Ser
                260                 265                 270

aga ggc tgc gtg cag gaa gaa atc cgg ttc atg ata aac cca gaa ttg      864
Arg Gly Cys Val Gln Glu Glu Ile Arg Phe Met Ile Asn Pro Glu Leu
            275                 280                 285

atc gtg ggc atg ctc ttc atg gtt tca atg gaa gat aat gaa gct ata      912
Ile Val Gly Met Leu Phe Met Val Ser Met Glu Asp Asn Glu Ala Ile
            290                 295                 300

gaa att gtt ggt gca gaa agg ttc tca cag tac atg ggg tat ggt tcc      960
Glu Ile Val Gly Ala Glu Arg Phe Ser Gln Tyr Met Gly Tyr Gly Ser
305                 310                 315                 320

tca ttc cgt ttt act ggt gac tac tta gat agc aaa ccc ttt gat gcg     1008
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Ser Phe Arg Phe Thr Gly Asp Tyr Leu Asp Ser Lys Pro Phe Asp Ala
                325              330              335

atg ggt aga cgg aaa act agg ata gtg gca att gat gct ttg gac tgt    1056
Met Gly Arg Arg Lys Thr Arg Ile Val Ala Ile Asp Ala Leu Asp Cys
            340              345              350

cca act agg tta cag ttt gaa tct agt ggt ctt cta agg gaa gtg aac    1104
Pro Thr Arg Leu Gln Phe Glu Ser Ser Gly Leu Leu Arg Glu Val Asn
            355              360              365

aag gct ttt tgt gga ttt ttg gat caa tca aat cat cag ctc tgt gca    1152
Lys Ala Phe Cys Gly Phe Leu Asp Gln Ser Asn His Gln Leu Cys Ala
            370              375              380

aag ctt gtc cag gat tta aat aca aag gat aac tgt cca agt gtc att    1200
Lys Leu Val Gln Asp Leu Asn Thr Lys Asp Asn Cys Pro Ser Val Ile
385              390              395              400

cct gat gaa tgc ata gga gtt tca act gga aac tgg ggt tgc ggg gct    1248
Pro Asp Glu Cys Ile Gly Val Ser Thr Gly Asn Trp Gly Cys Gly Ala
                405              410              415

ttt ggt gga aac cct gaa atc aag agc atg att caa tgg att gct gca    1296
Phe Gly Gly Asn Pro Glu Ile Lys Ser Met Ile Gln Trp Ile Ala Ala
                420              425              430

tca cag gca ctc cga tct ttt att aac tac tac act ttt gag tcc gaa    1344
Ser Gln Ala Leu Arg Ser Phe Ile Asn Tyr Tyr Thr Phe Glu Ser Glu
            435              440              445

tca ctg aaa aga tta gaa gag gtg acc cag tgg ata ttg cgc cat agg    1392
Ser Leu Lys Arg Leu Glu Glu Val Thr Gln Trp Ile Leu Arg His Arg
            450              455              460

tgg acg gtt ggc gag ttg tgg gac atg ctt gtg gag tat tca tcc cag    1440
Trp Thr Val Gly Glu Leu Trp Asp Met Leu Val Glu Tyr Ser Ser Gln
465              470              475              480

agg cta aga gga gac acc aat gag ggc ttt tta aca tgg cta ctt ccc    1488
Arg Leu Arg Gly Asp Thr Asn Glu Gly Phe Leu Thr Trp Leu Leu Pro
                485              490              495

aag gac atc ccc aat ggt gat gta gat tac atg tgt gaa tag           1530
Lys Asp Ile Pro Asn Gly Asp Val Asp Tyr Met Cys Glu
                500              505


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<400>   16

Met Glu Ala Arg Gly Asp Leu Arg Ser Ile Leu Pro Tyr Leu Pro Val
1               5               10              15
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21

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Val Leu Arg Gly Gly Ala Leu Phe Trp Pro Pro Ala Ala Gln Glu Ala
         20                  25              30

Leu Lys Ala Leu Ala Leu Gly Pro Asp Val Ser Arg Val Ser Ser Gly
         35                  40              45

Asp Val Leu Ala Asp Ala Leu Thr Asp Leu Arg Leu Ala Leu Asn Leu
     50                  55              60

Asp Pro Leu Pro Arg Arg Ala Ala Glu Gly Phe Ala Leu Phe Phe Asp
65                  70              75                  80

Asp Leu Leu Ser Arg Ala Gln Ala Arg Asp Trp Phe Asp His Val Ala
             85              90                  95

Pro Ser Leu Ala Arg Leu Leu Leu Arg Leu Pro Thr Leu Leu Glu Gly
         100             105             110

His Tyr Arg Ala Ala Gly Asp Glu Ala Arg Gly Leu Arg Ile Leu Ser
         115             120             125

Ser Gln Asp Ala Gly Leu Val Leu Leu Ser Gln Glu Leu Ala Ala Ala
     130             135             140

Leu Leu Ala Cys Ala Leu Phe Cys Leu Phe Pro Thr Ala Asp Arg Ala
145             150             155                 160

Glu Ala Cys Leu Pro Ala Ile Asn Phe Asp Ser Leu Phe Ala Ala Leu
             165             170             175

Cys Tyr Asn Ser Arg Gln Ser Gln Glu Gln Lys Val Arg Cys Leu Val
             180             185             190

His Tyr Phe Asp Arg Val Thr Ala Ser Thr Pro Thr Gly Ser Val Ser
         195             200             205

Phe Glu Arg Lys Val Leu Pro Arg Arg Pro Glu Ser Asp Gly Ile Thr
     210             215             220

Tyr Pro Asp Met Asp Thr Trp Met Lys Ser Gly Val Pro Leu Cys Thr
225             230             235                 240
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Phe Arg Val Phe Ser Ser Gly Leu Ile Glu Asp Glu Glu Gln Glu Ala
            245                 250                 255


Leu Glu Val Asp Phe Ala Asn Arg Tyr Leu Gly Gly Gly Ala Leu Ser
            260                 265                 270


Arg Gly Cys Val Gln Glu Glu Ile Arg Phe Met Ile Asn Pro Glu Leu
            275                 280                 285


Ile Val Gly Met Leu Phe Met Val Ser Met Glu Asp Asn Glu Ala Ile
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Glu Ile Val Gly Ala Glu Arg Phe Ser Gln Tyr Met Gly Tyr Gly Ser
305                 310                 315                 320


Ser Phe Arg Phe Thr Gly Asp Tyr Leu Asp Ser Lys Pro Phe Asp Ala
            325                 330                 335


Met Gly Arg Arg Lys Thr Arg Ile Val Ala Ile Asp Ala Leu Asp Cys
            340                 345                 350


Pro Thr Arg Leu Gln Phe Glu Ser Ser Gly Leu Leu Arg Glu Val Asn
            355                 360                 365


Lys Ala Phe Cys Gly Phe Leu Asp Gln Ser Asn His Gln Leu Cys Ala
    370                 375                 380


Lys Leu Val Gln Asp Leu Asn Thr Lys Asp Asn Cys Pro Ser Val Ile
385                 390                 395                 400


Pro Asp Glu Cys Ile Gly Val Ser Thr Gly Asn Trp Gly Cys Gly Ala
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Phe Gly Gly Asn Pro Glu Ile Lys Ser Met Ile Gln Trp Ile Ala Ala
            420                 425                 430


Ser Gln Ala Leu Arg Ser Phe Ile Asn Tyr Tyr Thr Phe Glu Ser Glu
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Ser Leu Lys Arg Leu Glu Glu Val Thr Gln Trp Ile Leu Arg His Arg
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gcgcgggcta gatgggttgc gatggtcgtc ttgcctgacc cgcctttctg gttaagtaca   9960

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